

Application No.: 09/857,612

Docket No.: BB-1262

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Amendments to the Specification:**Paragraph at page 3, line 32 to page 4, line 4:**

Figures 1A and 1B depict ~~Figure 1 depicts~~ the amino acid sequence alignment between the lecithin:cholesterol acyltransferase corn clone cen3n.pk0141.f2:fls (SEQ ID NO:8), corn clone cep1c.pk001.f7:fls (SEQ ID NO:10), corn clone chpc24.pk0001.c1 (SEQ ID NO:12), and soybean clone sl2.pk0015.e8:fls (SEQ ID NO:14), with the *Arabidopsis thaliana* lecithin:cholesterol acyltransferase protein (NCBI General Identifier No. 3935185; SEQ ID NO:15). Conserved sequence elements are shown boxed in black with the amino acid sequence in white. The second boxed sequence (HS*G) contains a conserved serine that is believed to be the active site residue found in all serine lipases. This sequence motif is also conserved in mammalian lecithin:cholesterol acyltransferases (Rogne et al. (1987) *Biochem Biophys Res Commun* 148:161-169). All of the boxed sequences are largely conserved in the mammalian lecithin:cholesterol acyltransferase sequences.

Paragraph at page 20, line 31 to page 21, line 2:

Figures 1A and 1B present ~~Figure 1 presents~~ an alignment of the amino acid sequences set forth in SEQ ID NOs:8, 10, 12, and 14, and the *Arabidopsis thaliana* sequence (SEQ ID NO:15). The data in Table 4 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:8, 10, 12, and 14, and the *Arabidopsis thaliana* sequence (SEQ ID NO:15).